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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool/US09765034/runat_05122002_132015_21439/app_query.fasta_1.519
-Q-/cgn2_1/USPTO_spool/US09765034/runat_05122002_132015_21439/app_query.fasta_1.519
-DB-GenEmbl -QFWT=fastap -SUFFIX-p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MAXILEN-200000000
-USER-US09765034_@CGN_1_1_1616_@runat_05122002_132015_21439 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Fgapop 6.0 , F
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_ram:*
36: em_htg_ram:*
37: em_htg_vrt:*
38: em_sy:*
40: em_htgo_num:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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444 443 544 544 544	3332287 33322887 33322887	120	4664000	No.
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           ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg
                                              CTGGAAAAGTACCTTTCCATTTTTATGGGATTGAGTTCGTTGGGAGTCCTTGGA
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GTGCTTCATGCCAACCTCTATACCAGCATTCTCTCTCTCACTTTTATCAGCATAGATCGA
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Zhang,W., Li.N., Wan,T. and Cao,X.
Direct Submission
Submitted (21-MAR-2000) Department of Immunology, Second
Medical University & Shanghai Brilliance Biotechnology In
800 Xiangyin Rd., Shanghai 200433, P.R. China
Location/Qualifiers
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Zhang, W., Li, N., Wan, T.
Human P2Y purinoceptor
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INPVITDNGTFONDFASSGDRYNLIYSMCLTLGFILPLFVWGFYYKIALFLKQRN
RQVATALPLEKPLNLVIMAVVIFSVLFTPYHVMRNVRIASRLGSWKQYQCTQVVINSF
RVTTRPLAFLNSVINPVFYFLLGDHFRDMLMNQLRHNFKSLTSFSRWAHELLLSFREK
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/db_xref="taxon:9606"
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Mammalia; E
                                                    Submitted (08-FEB-2001) Entwicklungsneurobiolog:
                                                                                  Wittenberger, T
                                                                                                                   Wittenberger, T., Schaller, H.C. and Hellebrand, S. An expressed sequence tag (EST) data mining strategy the discovery of new G-protein coupled receptors J. Mol. Biol. 307 (3), 799-813 (2001)
                                                                        Direct Submission
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ttenberger, T., Schaller, C.H.
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/db_xref="taxon:9606"
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            PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln
                                                          ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu
                                                                                            IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp
                                                                                                                                          TTAATCTCCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTT
                                                                                                                                                      LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeu
                                                                                                                                                                                                      TyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIle
                                                                                                                                                                                                                                                     ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg
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TALPLEKPLNLVIMAVVIFSVLFTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVT
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YTSILFLTFISIDRYLLIKYPFREHLLØKKEFAILISLAIWLLVTLEILPILNPV
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/note="orphan receptor"
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SOURCE
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http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                               Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.g. Series: IRAL Plate: 41 Row: e Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1478
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Direct Submission
Submitted (03-JUN-2002) National Institutes of Health, Mammalian Submitted (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-renail.nih.gov
Tissue Procurement: CLONTECH
                                                                                                                                                                                                                                                                                                              Dickson, M.,
R. M.
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Mammalia; ]
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BC030948.1 GI:21410927
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100...1104
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                                                                                                                                                                   1. .1449
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YIVTRPLAFLNSVINPVFYFLLGDHFRDMLMNQLRHNFKSLTSFSRWAHELLLSFREK
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1585 AGCAGATGGGCTCATGAACTCCTACTTTCATTCAGAGAAAAG

AC116026 LOCUS COMMENT REFERENCE REFERENCE REFERENCE SOURCE KEYWORDS VERSION ACCESSION DEFINITION RESULT 6 AUTHORS TITLE JOURNAL TITLE JOURNAL AUTHORS JOURNAL TITLE AUTHORS ORGANISM Barbarla, J., Benton, J., Binage, R., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burch, K.L., Bydd, N.C., Chen, G., Chen, R., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Garner, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Garris, C., Harris, K., Hatt, M., Haylak, P., Hawes, A., He, X., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Kelly, S., Khan, U., King, L., Korvah, J., Jackson, E., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Jackson, E., Karlsson, B., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovuc, J., Kureshi, A., Landry, N., Leal, B., Levis, L., Li, J., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Massey, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Maylan, P., Martin, R., Martindale, A., Martinez, E., McLeod, M.-P., Meador, M., Melor, S., Morgan, M., Moorish, T., Morris, S., Moser, N., Neal, N., Vetason, D., Newtson, N., Nguyen, A., Nguyen, N., Pace, A., Payton, B., Pecry, J., Perzy, J., Taylor, C., Taylor, T., Peters, L., Shooshtari, N., Sisson, I., Sodergren, E., Sonal Re, T., Shooshtari, N., Tang, O., War, Marc, M., Saytek, A., Tangey, J., Taylor, C., Watlingson, A., Wall, N., Nakar, M. Worley, K.C.

Direct Submission

Submitted (23-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One of Molecular and Turn Plaza, Houston, TX 77030, USA Submitted (09-APR-2002) Human Genome Sequencing Center, of Molecular and Human Genetics, Baylor College of Medic Baylor Plaza, Houston, TX 77030, USA INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu Worley, K.C. Direct Submission Gibbs, R. Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 90343) AC116026 90343 bp DNA linear PRI 09-APR-20 Homo sapiens 3 BAC RP11-3F11 (Roswell Park Cancer Institute Human BAC Library) complete sequence. Direct Submission Unpublished Homo sapiens AC116026.1 (bases 1 to 90343) GI:19697319 Medicine, PRI 09-APR-2002 Banks,T., Allen,C., Department

> CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are c sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. only

ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome of a local database that includes entries local mapping efforts. Res. 7:541-550) searches from dbSTS, GDB, and

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequences similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

OUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

FEATURES repeat_region source QUALSTAT-REPORT. /rpt_family="FLAM_C" 5657. .5762 /rpt_family="LTR21B" 6289. .6773 /rpt_family-"L1MC/D" 5906. .6237 complement(15157 complement(8725. . /rpt_family="AluSx" complement(3048. .3 complement(2742. /rpt_family="Aluy" complement/or/^ complement(1314 /rpt_family="L1M4" complement/27/2 /rpt_family="HERVFH21" /rpt_family-"Alusx" /rpt_family="MER45B" /clone="RP11-3F11" /db_xref="taxon:9606" Location/Qualifiers 'standard organism="Homo sapiens" _family="L2" _family="MER11D" family="(TA)n" family-"AT_rich" family="Alu" name="136046" .15633) 1627)

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complement(18376. . 18471)
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25783. .2
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22685. .23013
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                                                                                   Submitted (29-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                           Submitted (28-MAR-2002) of Molecular and Human (Baylor Plaza, Houston, (bases 1 to 132745)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (26-MAR-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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Submitted (25-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Havlor Plaza, Houston, TX 77030, USA
                  of Molecular and Human Genetics, Baylor College of Medicine Baylor Plaza, Houston, TX 77030, USA On Mar 28, 2002 this sequence version replaced gi:19718616. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu
                                                                                                                       Submitted (24-JUL-2002) Human Genome Sequencing
                                                                                                                                                   Direct Submission
                                                                                                                                                                        Worley, K.C.
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                                                                                               Center, Depa
of Medicine,
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sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are Features listing. clones are only

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

OUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at NRL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

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FEATURES
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                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 158144)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
2 (bases 1 to 158144)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.
Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
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AC016455
AC016455.2 GI:7381788
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TITLE JOURNAL COMMENT

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Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Mcdonald, P., Marguis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (30-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 1, 2000 this sequence version replaced gi:6479070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is
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Web site: http://www-seq.wl.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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44 42343: gap of 10
44 44474: contig of 2
75 44574: gap of 10
75 48293: contig of 3
74 48393: gap of 10
74 53132: contig of 4
75 53232: gap of 10
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39 28558: gap of 100 bp
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                                                                                  /note="assembly_fragment" 42344. .44474
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63120: contig of 5148 b
3220: gap of 100 bp
68799: contig of 5579 b
8899: gap of 100 bp
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358: gap of 100 bp
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85094: contig of 5945 bp in length
194: gap of 100 bp
19567: contig of 5373 bp in length
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372: gap of 100 bp
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74014: contig of 5115 bp in length
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                                      GlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsn
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85195. .90567
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63221. .68799
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57973. .63120
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96359. .103095
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AX376573
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                           house mouse
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Rodentia;
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          LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla
                                                                ATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTAC
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Mammalia; Eutheria; R
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Wittenberger, T., Scha
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Submitted (14-AUG-2000) ZMNH, Institut
Entwicklungsneurobiologie, Martinistr.
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camaratta, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
                                                                                                                                                                         1 (bases 1 to 60298)
Birren,B., Linton,L., Nusbaum,C.
Birsen,B., Linton,L., Nusbaum,C.
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AUS clone RP24-540E9,
AC116149
AC116149.1 GI:19703273
HTG; HTGS_PHASE0.
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                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                              Unpublished
                                                                                                                                          (bases 1 to 60298)
                                                                                                                                                                                                                                                                          musculus.
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9, LOW-PASS SEQUENCE SAMPLING.
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2398 3097: gap of 100 bp
2998 3097: gap of 100 bp
3098 3786: contig of 689 bp
3787 3886: gap of 100 bp
4577 contig of 680 bp
4577: gap of 100 bp
4578 4677: gap of 100 bp
5358 5457: gap of 100 bp
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5458 6150: contig of 693 bp
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Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                           * NOTE: This record contains 77 individual
* sequencing reads that have not been assembled into
* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for.
identifying clones that may be gene-rich and allows
'identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Research, 320 Charles Street, Cambridge, MA 02141, US All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-MAR-2002) Whitehead Institute/MIT Center
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Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                preserved.
b56: contig of 656 bp in length 100 bp 1426: contig of 670 bp in length 6. Gas of 670 bp in length
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94 18693: gap of 100 bp in 1e 162 2527; gap of 100 bp in 1e 152 2734; contig of 687 bp in 1e 152 27328; contig of 697 bp in 1e 152 27346; contig of 698 bp in 1e 152 27346; contig of 699 bp in 1e 152 27346; cont
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ω ¬	>AsnGlyThrThrCysA : ::: \GAGGGCAGTAACTGCA	alIleThrAs - TCCCAAAAGA	□ :0	CITT	LeuLeuProlle: ::: STTCTACCCATG	154 Le :: 4330 GT	Qy	
153 432	TrpValLeuValThrLeuGlu TGGGCCTTAGTGACCTTAGAA	erLeuAlaIleTrp ::: CGCTGGCTGTCTGC	leLeuIleSerL TTTAATCTCGC	Sluphealaile SAATTTGCCATT	BlnLysLysGlu CAAAAGAAGGAA	134 G1 4270 CA	Оy	
133 426	ProPheArgGluHisLeuLeu 	leLysTyrPr :: TGAAGTACCC	:gTyrLeuIleI :::: ATATCTGCTCA	IleAspArg ::: ATGGACCGA	PhelleSer TCATTAGO	114 Thr 4210 ACT	Qу	
113 420	TThrSerIleLeuPheLeu 	laAsnLeuTyrThrs CCAACCTCTACACC <i>I</i>	ArgTyrValLeuHisal CGATATGTGCTTCACAC	CASDATGTYT CAACCGATAT	LeuCysIleSer	94 Le 4150 CT	Qу	
93 414	AsnGlyAsnTrpIleTyrGlyAspVal AATGATAAGGGGACCTATGGAGATGTT	laAsnGlyAs CCAATGATAA	ArgSerTyrAla ::: AAGAGTTATGCC	MetLeuIleArgSerTy ::: ::: ATCCTGATAAAGAGTTA	ThrLeuPro	74 Cys 4090 TGC	Qy	
73 408	lSerAspLeuAlaPheLeu 	snLeuSerVa :: ACCTTTCCAT	erAsnIleTyrLeuPheAsnLeuSerValSe ::: CAATGTCTATCTTTTAACCTTTCCATCTC	SerAsnIle ::: AGCAATGTC	rpAsnSer 3GAACAGC	54 AsnT: 4030 AACTO	Qy Db	
53 402	YTYrIlePheSerLeuLys	TleValValTyrGlyTyr ::: ACTGTGGTGTTTGGCTAC	AsnThr AATGTC	lyValLeuGly ::: GACTGCTTGGG	ValValo ;;; ATTTTT	34 Phe 111 3970 TTC	Оу	
33 396	rIlePheTyrGlyIleGlu TGCATTTTATGCAATCGAG	TrLeuSe	LeuGluLysTyrTy !TTGAATAAGTACT!	LuAlaAla :: \GGCTATC	TrpLeuAlaAlaGl GGTGGAATTCTC!	14 Tr 3910 Tg	Qy db	
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	in length in length	100 bp 100 bp f 699 bp 100 bp	contig c	53267: gap 53266: 53966: 54066: gap	* * 53168 * 53268 * 53967			
	leng	100 bp	contig	52484: g	5168 5238			
	leng	100 bp	of	. 0	5090			
	gt	100 bp	contig	Ö i	5001 5001			
	in length	100 bp	contig	46331: 9 49221 49321: a	4953			
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren,B., Linton,L., Nusbaum,C. and Lander,E. Mus musculus, clone RP24-540E9
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AC116149
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                NOTE: This record contains 77 individual
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                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L24912

Center clone name: 540_E_9
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9, LOW-PASS SEQUENCE SAMPLING.
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However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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16248 16347: gap of 681 bp
17029: 17128: gap of 100 bp
17129 17128: gap of 674 bp
17129 17902: gap of 100 bp
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21751: contig of 677 bp
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3197: gap of 100 bp
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1057: contig of 680 bp
457: gap of 100
6150: contig
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67: gap of 691 1
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26357: contig
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Eukaryota; Metazoa;
Mammalia; Eutheria;
           Bell, G.I.
Direct Submission
                                                     Tokuyama,Y., Hara,M., Jones,E.M., Fan,Z. au
Cloning of rat and mouse P2Y purinoceptors
Biochem. Biophys. Res. Commun. 211 (1), 21:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GRLKKKNAIYYSVLVWLIVVALSFULFYSGTGTRKNKTYTCYDTTSNDYLRSYFIYE
MCTTVAMFCIPLVLILGCYGLIVKALIYNDLDNSPLRRKSIYLVIIVLTVFLAGDTFRRR
HYMKTMMLRARLDFOTPEMCDFNDRVKATYQVTRGLAGLNSCVDPILYFLAGDTFRRR
                LSRATRKASRRSEANLQSKSEEMTLNILSEFKQNGDTSL
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/db_xref="taxon:10090"
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                                                                                                                        ValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySer
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                                                                                               GTGTCTTATATCCCTTTCCATGTGATGAAAACGATGAATTTGCGAGCACGGTTG-----
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/gene="P2Y1"
9721. .9727
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                                                                                                                                                                                                                                                                                                                      /translation="MTEVPWSVVPNGTDAAFLAGLGSLWGNSTVASTAAVSSSFQCAL
TKTGFGPYYLLAVYILVFIIGFLGNSVALWMWYHMKWWSGISYWMFNLALADFLYVL
TLPALIFYYENKTDWIEDDAWCKLGNETFHVNLYGSILFLTGISAHRYSGVVYPLKSL
GRLKKKNAIYVSVLVWLIVVVAISPILFYSGTGTRKNKTVTCYDTTSNDYLRSYFIYS
MCTTVAMFCIFLVLIIGGYGLLVKALIYNDLDNSPLRRKSIYLVIIVLTVFAYSYIPF
HVMKTMNLRARALDFQTFEMCDENDRYVATYQYTYRGLASLNSCVDPILYFLAGDTFRRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="P2Y1 receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="P2Y1"
/function="ADP receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sub_species="mus musculus"
/db_xref="taxon:10090"
/cell_line="ES 129/Sv D3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3251 GTGTTCATCATAGGCTTCCTAGGCAACAGCGTGGCTATCTGGATGTTCGTTTTCCACATG 3310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3191 CAATGTGCCCTGACCAAGACCGGTTTCCAGTTCTACTACCTGCCGGCTGTCTACATTTTA 3250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3131 CTGGGCTCGCTTTGGGGAAACAGTACTGTCGCCTCAACTGCAGCAGTTTCCTCTTCATTC 3190
4049 GCTGGAGATACATTCAGAAGGAGACTGTCCCGAGCCACCAGG 4090
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                                                                                                                                                                                                                                                                                                                         CysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThr 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluPheValValGlyValLeuGlyAsnThrIleValValTyrGlyTyrIlePheSerLeu 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGCCATCTCCCCTATTCTCTTCTACTCTGGCACTGGGACTCGGAAAAAACAAAACTGTC 3670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCCTCACCTGCATCAGCGCACACAGGTACAGTGGCGTGGTGTACCCTCTCAAGTCTCTG 3550
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                                                                                                                                                                         GTGTCTTATATCCCTTTCCATGTGATGAAAACGATGAATTTGCGAGCACGGTTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuCysThrLeuProMetLeuIleArgSerTyrAlaAsn---GlyAsnTrpIleTyrGly 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluAlaAlaLeuGluLys------TyrTyrLeuSerIlePheTyrGlyIle 32
                                                                          IleValThrArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeu 297
                                                                                                                                                                                                     ValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySer 262
                                                                                                                                                                                                                                                    AlaLeuProLeu---GluLysProLeuAsnLeuValIleMetAlaValIValIlePheSer 242
                                                                                                                                                                                                                                                                                                                                                                          ThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeu 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuGlyAspHisPheArgAspMetLeuMetAsnGlnLeuArg 311
                                                                                                                                              TrpLysGlnTyrGlnCysThrGlnValVal------IleAsnSerPheTyr 277
                                                                                                                                                                                                                                  -----CCGCTCCGGAGGAAATCCATTTACCTGGTGATAATTGTCCTGACGGTGTTTGCT
                                                                                                                                                                                                                                                                                               TGTTATGGATTAATTGTTAAAAGCTTTGATTTACAATGACCTGGACAACTCT------
                                                                                                                                                                                                                                                                                                                                                            ATCTACAGTATGTGCACGACTGTGGCCATGTTCTGCATCCCTTTGGTGCTGATCTTGGGC 3775
                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTGCTATGACACCACGTCCAATGATTACCTGCGAAGT-----TATTTC 3715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuGluLeuLeuProIleLeu------ProLeuIleAsnProValIle 165
                                                                                                               ----GATTTCCAGACCCCAGAAATGTGTGATTTCAACGACAGGGTTTATGCCACTTAT
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